## SUBJECT INDEX

A	Aspergillus flavus, aflatoxin formation epidemiology,	evidence for physiologic specialization, 363-65
Abscisic acid  Phytophthora infected plants,	249-70 biology, 250-51	pathogenicity variation, 361-69
221	dispersal, 252	pathogenic specialization,
Acremonium	factors influencing infection	362
coenophialum, 295, 301,	and aflatoxin formation,	shifts in virulence 368-69
307-8	258	taxonomic status and
chemical control, 299	insect damage, 264-65	phenotypic variation,
detection by insect bioas-	moisture, 261-64	360-61
say, 298	other factors, 265-66	virulence in relation to bac-
endophyte origin, 307	substrate, 258	teriological properties,
ergot alkaloids, 306	temperature and time, 259-	369-70
fescue toxicosis, 300	61	disease resistance
growth of host, 303	introduction, 249-50	future prospects, 377-79
peramine, 305	mode of entry for infection	infection types, 374-75
serology, 297	boll sutures, 256	inoculation methods for re-
		sistance evaluation,
viability in seed, 298	developing fruit, kernels,	
lolii, 295-96, 301, 307-8	and seed, 256-58	370-71
chemical control, 299	flowers, 253-55	resistance genes, 375-76
endophyte origin, 307 growth of host, 303	stem, bract, and peduncle, 255	resistance mechanisms, 376-77
peramine, 305-6	primary inoculum, 251	resistance types, 371-74
ryegrass staggers, 300-1	secondary inoculum, 251-52	varietal resistance grouping,
serology, 297	Aspergillus nidulans, 95, 386	371
viability in seed, 298	transformation, 94	Baker, K. F., 71, 75
species	Aspergillus niger, 261, 265	Baker, R., 76, 80
symbiosis type, 302	Aspergillus flavus competitor,	Balansia
Acrolein, 238	262	epichloe, 301
Adenylate cyclase, 412 Aeciospores	Aspergillus parasiticus, 249 biology, 250	auxinlike compounds, 304 spp.
host penetration, 234	Atkinson, T. G., 74	animal toxicosis, 301
Aflatoxin	Atmosphere	symbiosis type, 301
see Aspergillus flavus, afla-	see Plant pathogens, modeling	Bancroft, K., 71
toxin formation	long-range transport in	Barrons, K. C., 68
epidemiology	the atmosphere	Basidiospores, 235
Agrobacterium	Atmospheric Transport and Dis-	Rhizoctonia
rhizogenes, 92	persion (ATAD) model,	epidemiological role, 137-
tumefaciens, 100, 160	170, 183	38
agrocin, 84, 101	atmospheric transport layer	rust fungi, 238-39
analogs of Rhizobium	definition, 171-72	appressoria, 237
genes, 151	model type, 179	host penetration, 233-34
host-range gene, 156	model verification, 184-85	Bean pod mottle virus, 113-
pathogenicity basis, 90-92	Auxin, 341	15
T-DNA vector, 97, 102-3	Azospirillum, 154	weed host importance, 116
Agrocin 84, 101	Azospiritum, 134	Bean rugose mosaic virus, 115
Ahmad, J. S., 80	В	Beetles
Alabouvette, C., 76	ь	
	D-b F D 46 40	see Viruses, beetle transmis-
Allen, M. C., 71	Babcock, E. B., 46, 49	sion
cAMP, 240, 243, 411	Bacterial blight of rice, 359-82	Belonolaimus spp., 330
Anderson, M. E., 54	description of the disease,	Benomyl, 299, 388
Anguina tritici, 327	359-60	Bentley, Robert L., 44
Appressorium	symptoms, 360	Biological control of plant
see Rust fungi, changes dur-	description of the pathogen	pathogens, 67-85
ing appressorium de-	controversy on physiologic	after 1965, 74-75
velopment	specialization, 362-63	cross-protection, 81
Armellaria mellea epidemiological studies, 395	differential systems for race identification, 365-68	effect of stress on host, 78-

effect of stress on microorganisms, 77-78 gene manipulation, 83-84 general suppression in suppressive soils, 75 growth-promoting rhizobiota, 82-83 hypovirulence, 81-82 integrated biological control, 76-77 nutrient base, 79 parasites of sclerotia, 82 possession principle, 77 protecting plant propagules, specific suppression in suppressive soils, 75-76 stress effects, 77 suppressive soils, 75, 138 thermal sensitivity of microbiota, 80 before 1965 cross-protection, 71-72 developments by 1934, 72fungistasis, 69 groundwork for new field, growth-promoting rhizobiota, 72 hypovirulence, 72 interactions of microorganisms, 67-69 integrated biological control, 70 nutrient base, 71 possession principle, 70-71 protecting plant propagules, rhizosphere studies, 69 stress effects, 71 suppressive soils, 69-70 thermal sensitivity of pathogens, 71 epilogue, 84-85 increase in published papers numbers, 74 introduction, 67 Rhizoctonia, 138 Biraghi, A., 72 Bitertanol, 299 Bliss, D. E., 70 Boots, William, 45 Börger, H., 71 Boswell, V. R., 73 Bradyrhizobium, 151 japonicum host-specific nodulation genes, 158 nod box, 153 Branching Atmospheric Trajectory (BAT) model, 170,

183

model type, 179 modeling the diffusion process, 176 wind shear, 172 Bremia lactucae, 387 multilocus genotypes, 393 probe source, 389 restriction fragment length polymorphism detection, 390 Broad bean stain virus, 114 seed-borne infection, 116 Broad bean true mosaic virus, seed-borne infection, 116 Broadbent, P. 75, 83 Broadfoot, W. C., 68 Bromoviruses, 112 Bruehl, G. W., 74 Bupirimate, 192 Burke, D. W., 78

Calcium, 240, 286, 407, 416 Calmodulin, 240 Cantaloupe salinity effect on fruit weight, 284 Carbendazim. 204 Carbon dioxide, 276 Carotovoricin, 413 Carroll, Jessie Anna, 48 Carter, M. V., 77 Cauliflower mosaic virus, 12, 16, 18 Cell wall-degrading enzymes, 31-33 Cellobiose, 418 Cellulase, 421 secretion, 419-20 Cellulose degradation, 418 Ceratobasidium, 126, 131 Chet, I., 76 Chinn, S. H. F., 69 Chitin, 239 Chitinase synthesis gene, 101 Chlamydospores, 322-23, 326 Chloride, 275, 278, 283, 286 seasonal change in peanut, 279-80 Chrysomelidae, 113 Clavibacter, 148 Claviceps purpurea, 386 Clavine, 300

Coccinellidae, 113

Comoviruses, 112

95, 386-88

Coley-Smith, J. R., 78

Cochliobolus heterostrophus,

Cocksfoot mottle virus, 113

Aspergillus, 251-54, 256 Cook, R. J., 77-78 Corn Aspergillus aflatoxin formation, 260-63, 265 invasion, 253-54, 257 salinity effect osmotic potential, 273 water potential, 274 Corticum microsclerotia, 133 Costa, A. S., 81 Cotton Aspergillus aflatoxin formation, 261, 263-66 invasion, 254-58 Cowpea aphid-borne mosaic virus, 117 Cowpea chlorotic mottle virus transmission, 117 Cowpea mosaic virus, 13 Cowpea severe mosaic virus, 115, 117 host effect upon spread, 116 weed hosts, 116 Cruickshank, I. A. M., 71 Cucumber mosaic virus, 13, 103 inactivation by RNase, 118 Curculionidae, 114 Cutinase gene, 95-96 Cyanide, 342-45, 350-51 Cycloheximide, 388 Cytokinins, 330 Phytophthora-infected plants,

Darling, H. M., 53

Day, P. R., 82

Conidia

Deuterium oxide, 242 Dickson, J. G., 53 Dilophospora alopecuri, 327 Disease control, relation of art and science conclusion, 7-8 etiology, 2-7 concept, 2-5 introduction, 1 separating art from science, Disease resistance, 34-37 induced resistance, 37-39 DNA base composition Rhizoctonia, 134 restriction fragment length polymorphisms see Genetic analysis of phytopathogenic fungi

sequence homology Rhizoctonia, 134-35 mtDNA, 385-86 Dobbs, C. G., 69 Duggar, B. M., 55

E

Elasmopalpus lignosellus, 264 Endothia parasitica dsRNA, 386 Epichloe typhina, 295, 305 detection, 297 distribution in plant, 302 effects on plant growth, 304 evolution, 308 symbiosis type, 301-2 Ergonovine, 305, 307 Ergot alkaloids, 300, 305-6 Ergotamine, 305, 307 Ergovaline, 300, 305 Erysiphe graminis, 194, 201-3 Erwinia amylovora, 147, 158 carotovora, 151 pectate lyase genes, 93 carotovota subsp. atroseptica, 405 pectate lyase effect on plant tissues, 415 pectate lyase genes, 409-10 pectate lyase isozymes, 407, 409 pectin lyases, 410 polygalacturonase, 410 carotovora subsp. betavasculorum, 405 carotovora subsp. carotovora, 405, 416, 421, 423 cellulose degradation, 418 hemicellulases, 419 lipopolysaccharide, 421 pectate lyase effect on plant tissues, 415 pectate lyase genes, 408-9, 420 pectate lyase isozymes, 407-8, 414 pectate lyase synthesis regulation, 411 pectin lyases, 410 pectin lyase synthesis regulation, 413 polygalacturonase, 410, 422 polygalacturonase role in virulence, 415 proteases, 418-19 chrysanthemi, 405 cellulase and pectinase secretion, 419-20

cellulose degradation, 418

hemicellulases, 419

iron acquisition and pathogenicity, 422 lipopolysaccharide, 421 pectate lyase effect on plant tissues, 415-16 pectate lyase genes, 93, 408-9, 410 pectate lyase induction, 411 pectate lyase isozymes, 407-8, 410, 414, 416, 422 pectate lyase synthesis regulation, 411-13 pectinases role in virulence, 414-15 pectin lyases, 410, 419 pectin lyase synthesis, 413 pectin methylesterase gene, proteases, 418-19 cypripedii, 405 rhapontici, 405 rubrifaciens, 422 Essig, E. O., 49-50 Ethirimol, 192 Ethylene, 341 Exopolysaccharide, 158-61

F-actin, 235-36, 242 Farlow, W. G., 43 Fenpropimorph apparent activity and inoculum density, 198 Fescue toxicosis, 300 Filamentous distalsome, 235 effect on Phytophthora cinnamomi, 214 Fleming, A., 68 Flor, Harold Henry, 59-66 contributions, 61-65 early years, 59-61 introduction, 59 the man, 65-66 Fokkema, N. J., 79 Fox, R. A., 71 Fulbright, D. W., 82 Frankia, 154 Fungal endophytes of grasses, 293-315 animal toxicities, 299-300 Balansia-infected weed grasses, 301 fescue toxicosis, 300 ryegrass staggers, 300-1 concluding remarks, 309-10 grass-fungus interactions benefits to the fungus, 302 benefits to the host, 303-7 disease resistance, 307 growth of host, 303-4

insect species affected, 304 origins, 307-8 parasitic and mutualistic symbiosis, 301-2 tolerance to grazing herbivores, 307 tolerance to insect herbivores, 304-7 historical perspectives, 294 chemical control, 299 classification, 295 control methods, 298-99 culture of fungi, 297-98 detection methods, 296-98 heat effect, 298 incidence, 295-96 insect bioassay, 298 mycelium staining, 297 seed storage effect, 298 serology, 297 introduction, 293-94 use of infected and noninfected grasses, 308 endophyte-free cultivars, 308-9 endophyte-infected grasses, 309 phytopathogenic fungi

Fungi see Genetic analysis of Fungicide screening, 189-206 choice of organisms, 192-94 fungicides used in world agriculture, 191 proportion used on different crops, 192 future developments, 204-5 introduction, 189 objectives and economic considerations, 189-90 procedures for further evaluation

bioassay for systemic and vapor activity, 203 dew, 200 metabolism, 200-201 persistence, 199-201 rainfastness, 200 resistance, 204 translocation, 201 uptake and translocation, 201-4 UV light, 200

vapor activity, 201 volatility, 201 random screening and directed synthesis, 190-92

screen procedures application methods, 195 application rates, 194-95 assessment, 198-99 formulation, 194 humidity chambers, 196-97

inoculation, 197 inoculum density, 197-98 plant growth and incubation, 196 test unit and planting material choices, 195-96 Fusarium oxysporum see Fusarium wilt fungi and root-knot nematodes interactions, 317-38 oxysporum f. sp. apii populations variation, 396 oxysporum f. sp. conglutinans, 386 oxysporum f. sp. lycopersici effect of root-knot nematodes on host resistance, 331-33 solani f. sp. pisi cutinase gene, 95-96 Fusarium wilt fungi and rootknot nematodes interactions, 317-38 ecology and biology of fusarium wilt fungi, 321-25 disease symptoms, 323 host invasion, 322-23 host resistance types, 324host response to invasion, 323-24 hosts, 321 variation, 322 ecology and biology of rootknot nematodes, 319-21 effects on plants, 321 life cycle, 319-20 population composition, 319 survival, 319 symptoms of infected plants, 320 interrelationships, 325-26 interactions in the rhizosphere prior to penetration, 326-27 modification of host reaction to fungus, 331-32 nematode influence on fungus penetration and pathogenesis, 328-31 nematode vectors of fungal propagules, 327-28 introduction, 317-19

G

Gaeumannomyces graminis var. tritici, 353

summary and conclusions,

332-34

B-Galactosidase, 412-13 identification, 397 involved in bacteria-plant interactions, 162 Rhizobium common nodulation genes. 152-55 host-specific nodulation genes, 155-58 nod genes, 151-52 rice resistance to bacterial blight, 369, 373-76 sexual compatibility and vegetative incompatibility molecular markers, 387 soft-rot erwinias cellulose degradation, 418 pectate lyase, 408-13, 420 pectin methylesterase, 408 polygalacturonases, 410 protease, 419 virulence genes as markers, 387-88 Gene-for-gene relationship, 96, 146, 155 approaches to study, 98-100 molecular markers, 387 see also Flor, Harold Henry Genetic analysis of phytopathogenic fungi, 383applications of molecular markers asexual variation, 394 epidemiology and population genetics, 395-96 gene identification, 397-98 genetic bases of variation, 393-94 genetic maps, 388-93 genome organization and evolution, 392-93 integration with electrophoretic karyotype, 391-92 polymorphisms identification, 390 probe sources, 389-90 quantitative traits analysis, segregation analysis, 390-91 sexual variation, 393-94

taxonomy and phylogenetic relationships, 396-97 conclusions, 398-99 drug resistance and auxotrophic mutants, 388

introduction, 383-84 molecular markers advantages, 383 molecular markers isozymes, 384 double-stranded RNA, 386 mitochondrial DNA and plasmids, 385-86 restriction fragment length polymorphisms, 384-85 morphological markers, 386sexual compatibility and vegetative incompatibility genes, 387 virulence genes, 387-88 Genetics of pathogenesis by soft-rot erwinias, 405-30 conclusions and prospects, 422-23 extracellular enzymes, 418 cellulose degradation, 418 hemicellulases, 419 proteases, 418-19 host-parasite recognition, 420 iron acquisition role, 421 lipopolysaccharide role, 421-22 introduction, 405-6 pectinases of soft-rot erwinias, 406 pectate lyases, 406-10 pectin lyases, 410 polygalacturonases, 410 pectinases role in pathogeniceffects on plant, 415 expression in infected plant, 414 isozyme numbers, 416-17 requirement for virulence, 414-15 regulation of pectate lyase synthesis, 411 catabolite repression, 411-12 inducers, 411 negative control by gpiR gene, 412 negative control by kdgR gene, 412 negative control of pelA by pecR gene, 413 positive control by pecA gene, 412-13

regulation of pectin lyase syn-

thesis, 413 secretion of pectinase and cel-

Gerlagh, M., 76

Ghabrial, S. A., 72

lulase, 419-20

Gibberellins, 330	J	Meloidogyne
Gilbert, R. G., 78		arenaria
endo-β-1,4-Glucanase, 418	Jarrah dieback	races, 319
Glycine, 342, 344	see Phytophthora cinnamomi	hapla, 319
cGMP, 240	in Australasian forests	incognita, 328
Gold, Herb, 27	Jones, Henry A., 54-55	effect on tomato resistance
Grasses	Jones, L. R., 51	to Fusarium, 331-33
see Fungal endophytes of	Joslyn, M. A. 27	infected plants exudates
grasses	,,	effect on fungi, 326
Grente, J., 72, 81	K	races, 319
Grossbard, E., 68		javanica, 319
Growth-regulating substances,	Katan, J., 78	Fusarium in rhizosphere of
33-34	Keitt, G. W., 53	infected plants, 326
33-34	Kerr, A., 81	giant cells activity, 329-30
H	King, J. E., 78	host response to Fusarium-
n		
W	Klebsiella aerogenes	Meloidogyne infection,
Haenseler, C. M., 71	ribitol dehydrogenase gene,	329
Harman, G. E., 75	158	see also Fusarium wilt fungi
Hartig, Robert, 43	Kloepper, J. W., 83	and root-knot nematodes
Hartley, C., 68	Kojic acid, 250, 258	interactions, 320
HCN, 341-43, 351-53	Kommedahl, T., 75	Menzies, J. D., 70
Heat		MESOPUFF II, 170, 183
fungal endophytes control,	L	spore deposition velocity, 180
298-99		wind field selection, 172-73
Helminthosporium victoriae, 98	Larson, R. H., 53	Millard, W. A., 68
Hemicellulases, 419	Leach, R., 70	Mishustin, E. N., 72
Hemileia vastatrix, 237	Lectins, 149, 158-60, 239	Mitochondrial plasmids, 386
Henry, A. W., 68	Lindberg, G. D., 72	Mitomycin C, 410, 413
Heterobasidion annosum	Linderman, R. G., 78	Moffitt, E. M., 81
epidemiological studies, 395	Lindow, S. E., 79	Moisture
Hickmott, R., 45	Lipopolysaccharide	effect
		aflatoxin formation, 261-64
Hiltner, L., 69	role in pathogenicity, 421-22	
Hinson, W. H., 69	Lister, R. M., 81	jarrah dieback, 212
Hydathodes	Lochhead, A. G., 69	Molecular genetics impact on
Xanthomonas invasion route,	Loline alkaloids, 300, 305-7	plant pathology, 87-110
377	Lolitrems, 300-1, 306	basic principles and tech-
Hygromycin B., 95	Long-range transport of	niques, 87-90
Hypersensitive reaction	pathogens	complementary DNA, 89
Erwinia, 422	see Plant pathogens, modeling	cosmid vectors, 89
Rhizobium, 161	long-range transport in	DNA degradation, 88
Hypochnus sasakii, 127	the atmosphere	gene structure, 87-88
comparison with other Rhizoc-	Lycopodium	plasmid vectors, 88-89
tonia groups, 131	spores deposition velocity,	probes, 90
	180-82	transposons, 89
I		biological control
	M	bacteria, 100-2
Ice nucleation gene, 100		cross-protection by viruses,
Indole acetic acid, 324, 341	Magnaporthe grisea, 386-87	102-3
genes in Pseudomonas, 92-93	Maintenance respiration, 275	satellite RNA, 103
Infection strategies, 146-49	Maize chlorotic mottle, 113	viruses, 102
Inoculation methods	Manns, M. M., 70	future, 104
	Marx, D. H., 79	genetic basis of avirulence,
bacterial blight of rice, 370-		96-97
**	McBeth, C. W., 68	
Iron, 343-44, 346-48, 352	McClure, T. T., 72	genetic basis of disease resis-
acquisition role in pathogenic-	McKinney, H. H., 71	tance
ity, 421	Melampsora lini	genetic engineering of
Isozymes, 384-85, 393, 396	asexual variation, 394	plants, 97
pectate lyases, 407-10, 417-	avirulence genes as molecular	possible approaches to dis-
18, 422	markers, 387	ease resistance, 97-10
	F1-1	genetic basis of pathogenicity
in infected plant, 414	Flor's contributions, 61-65	genetic basis of patriogenieity
	heat shock proteins, 241	90

requirement for virulence,

415

fungi, 94-96 secretion, 420 soil characteristics, 212-13 separation and characterizatemperature, 211-12 genome sizes of organisms, tion of isozymes, 407host susceptibility and resisintroduction, 87 tance synthesis regulation, 411-13 pathogen detection, 103 interspecific resistance, Müller, G. W., 81 Pectin lyases, 410 221-22 Müller, K. O., 71 Pectin methylesterase, 406 intraspecific resistance, gene, 408 222-23 Mycotoxins, 249 Myriogenospora atramentosa, Pectinase, 421 introduction, 207-8 secretion, 419-20 management and control, 223-302 24 Pegg. K. G., 75 N Peramine, 305-7 mating type variability, 222-Peronosclerospora 23 philippinesis, 397 problems posed, 208-10 Nalidixic acid, 413 Naumova, A. N., 72 sacchari, 397 symptoms, 208 sorghi, 397 variable life cycle, 214-15 Nectria haematococca pisatin detoxification and Peronospora tabacina, 170, Pisatin, 95 175, 179 Plant growth-promoting rhizovirulence, 95 Neurospora crassa, 390, 397 spores bacteria Nigrospora oryzae, 261 modeling production and see Rhizosphere microorganisms, beneficial and de-Nitrate, 286 escape, 182 survivability, 180 Numerical weather-prediction leterious models, 185 Perrin, D. R., 71 Plant pathogens, modeling long-Phakopsora pachyrhiza, 233 range transport in the Phleum mottle virus, 113 atmosphere, 168-88 conclusions, 185 Phosphate, 286 Olsen, C. M., 71 Physiological plant pathology. numerical weather-Osmotic potential, 277 27-40 prediction models, 185 corn leaves and water salincell wall-degrading enzymes. data limitations to modeling, ity, 273 31-33 182-83 soil solution, 272 disease resistance, 34-37 introduction, 169-71 growth-regulating substances, ATAD model, 170 Oxygen ion uptake inhibition, 285 atmospheric boundary induced resistance, 37-39 layer, 170 introduction, 27-28 backward-in-time trajectorother subjects, 39-40 ies, 171 BAT model, 170 Papavizas, G. C., 77 toxins, 28-31 MESOPUFF II dispersion Peanut Phytoalexins, 34-38, 324 Aspergillus role in disease resistance, 94model, 170 insect damage effect on 95 trajectory analysis, 169 aflatoxin formation, Phytophthora model-calculated trajectories, 264-65 cinnamomi 171-73 multilocus genotypes, 393 modeling long-range transport invasion, 253, 256-57 moisture effect, 261-62 modeling considerations, infestans temperature effect, 259 asexual variation, 394 176-77 spore viability and deposichloride concentration, 279 isozyme loci variation, 393 seasonal change, 280 megakarya, 394 tion, 180-82 Pectate lyases megasperma transport models types, soft-rot erwinias, 406-7 variation, 397 177-80 catabolite repression, 411palmivora, 394 physical processes in the 12 Phytophthora cinnamomi in atmospheric boundary Australasian forests, 207-29 effect on plant tissue, 415 layer, 173-75 genes organization, 408-10 conclusion, 224-25 definition of ABL, 173 inducers of synthesis, 411 damage to the forest, 216-18 dispersion, 175-76 damage to the host, 218-21 isozymes expression in modeling the diffusion plant, 414 detection of disease and rate process, 176 isozyme numbers, 417-18 of extension, 215-16 thickness of ABL, 174 negative control, 412-13 distribution, 210-11 turbulence, 173-74 pathogenicity, 415-17 factors controlling disease, turbulence structure, 174-75 positive control, 412-13 211 verification of models, 184

fire, 214

moisture, 212

**Plasmids** 

mitochondria, 386

Meloidogyne interactions

root rot severity, 326-27

Rhizoctonia, 139 Podospora anserina, 386 Polygalacturonase, 410, 415, 417 Polygalacturonate, 411 cropping frequency and yield, 342-44 growth promoting pseudomonads, 346-48 interactions with deleterious rhizobacteria, 351 root colonization, 349 tuber treatment, 347 yield increase, 352-53 Potato spindle tuber disease, 14 Potassium, 238, 242, 278, 280 Potter, M. C., 67 Price, T. V., 77 Proline, 342, 345, 353 Pronase E, 239 Propiconazole, 299 Proteases, 418-20 Pseudobactin, 348, 351-52, 358 Pseudomonas fluorescens, 101, 351 root colonization, 349-50 putida, 102, 347-49, 351 root colonization, 350 solanacearum, 147, 158, 160-61 species, 342-43, 345, 352 chemotaxis, 349-50 plant growth-promoting strains, 346-48 survival on root residue, 353 syringae, 101, 148, 159 ice nucleation gene, 100 syringae pv. glycinea avirulence gene, 96-97 avirulence gene expression, 148 syringae pv. syringae, 348 syringae pv. tomato avirulence gene, 148 syringae subsp. savastanoi IAA genes, 92-93 Puccinia coronata, 98, 239 graminis appressorium formation, 238 isozyme loci variation, 393 uredospore germ tube orientation, 237 graminis f. sp. secalis gene flow, 396 graminis f. sp. tritici gene flow, 396 population genetics study,

graminis tritici, 239 heat shock, 241 hordeii, 372 psidii, 233 recondita f. sp. tritici, 395 striiformis, 386 **Pycniospores** host penetration, 234

biological bases of anastomosis and intraspecific grougs, 132 DNA base composition, 134 electrophoresis of proteins and isoenzymes, 133serological relationships, Ravenelia humphreyana, 233 133 Rawlins, T. E., 27 vitamin requirement, 132 Reinking, 70 conclusion, 139-40 Rem, L. T., 76 ecology and pathogenicity of Rhizobium, 145-68 groups, 135 avirulence determinants, 161 antagonism and biological control, 138 cell-surface oligosaccharides and polysaccharides role, breeding of resistant vari-158-61 eties, 137 common nodulation genes, epidemiological role of basidiospores, 137-38 152-55 genetic requirement for geographical distribution, nodulation, 151 135-36 host-specific nodulation host plants and distribution, genes, 155-58 136 definition, 156 plasmids, 139 hypersensitive reaction, 161 population fluctuations infection process summary, within a field, 136-37 148-49 dsRNA, 139 suppressive soils and disschematic representation, 150 ease decline, 138 infection strategies in plantviruses, 139 microbe interactions, intraspecific grouping, 127 146-48 hyphal anastomosis groupintroduction, 145-46 ing, 128-29 isolation and identification of hyphal fusion mechanism, nod genes, 151-52 129 leguminosarum, 151-52, 157, interrelations among various 159 groupings, 129 morphological and patholog host-range gene, 156 nodulation genes, 152-55 ical grouping, 127-28 melitoti, 152, 159 introduction, 125 host-specificity genes, 157-Rhizoctonia and Rhizoctonia solani 58 Rhizoctonia, 126 nodulation genes, 152-53, 155 Rhizoctonia solani, 126-27 phaseoli, 152 Rhizopus nigricans, 261, 265 refined parasitism, 161-63 Rhizosphere microorganisms, nod genes function, 162-63 beneficial and deleterious, 339-58 trifolii, 151-52, 159-60 host-range gene, 156-58 nodulation genes, 152-53, organisms, 345-46

beneficial rhizosphere micro-155 plant growth-promoting pseudomonads, 346-48 Rhizoctonia solani, ecology and root colonization, 348-50 pathogenicity, 125-143 anastomosis and intraspecific concluding remarks, 354 deleterious microorganisms groups importance, 131-32 cropping frequency effect, number of anastomosis 343-45 groups, 130 effect of cropping practices, teleomorphs, 130-31 343

identification, 340 mode of action, 341-43 terminology, 340 failures of growth promoting rhizobacteria, 352-54 interactions, 350-52 introduction, 339 Rhopalosiphum padi, 298 Rhynicosporum secalis, 394 Ribitol dehydrogenase gene, 158 see Bacterial blight of rice Rieman, G. H., 53 Riker, A. J., 53 Rishbeth, J., 70 **RNase** virus infection prevention, 118-19 dsRNA, 386 mRNA cross-protection, 102-3 Roberts, W., 67 Root exudates, 322, 326-27 Root-knot nematodes see Fusarium wilt fungi and root-knot nematodes interactions Rovira, A. D., 69, 72, 74 Russell, H. L., 51 Rust fungi, changes during appressorium development, 231-47 appressoria and subsequent infection structures, 232-33 aeciospores, 234 basidiospores, 233-34 pycniospores, 234 uredospores, 233 appressorium development inhibition, 242-43 differentiation and gene expression differentiation-specific genes, 242 protein synthesis, 240-41 elucidation of mechanisms, 243-44 introduction, 231-32 morphology and cytological development cytological changes after appressorium initiation, 236-27 nondifferentiated germ tube, 234-35 signal receptors for differentiation extracellular matrix, 239-40 second messengers in differentiation, 240

triggers and signals for de-

velopment initiation

thigmodifferentiation, 237-Ryegrass staggers, 300-1 Saccharomyces cerevisiae, 390 Salmonella typhimurium, 154 Salt tolerance and crop production, 271-91 detrimental effects of salinity, 271-72 energy costs, 275 nutritional effects, 274-75 plant growth, 272 protective mechanisms against salinity, 276 water relationships, 272-74 introduction, 271 protective mechanisms, 276 against ion toxicity, 277-81 against tissue water loss, 276-77 figure, 277 strategies for crop production, 281-82 approaches to breeding and selection, 283 crop management approach, 281-82 fertilization, 285-86 genetic manipulation, 282-84 grafting, 285 hormone application, 286 nutritional approach, 285 oxygen enrichment, 285 salinity as an advantage, 286 summary, 286 Sanford, G. B., 68-69 Sauret, S., 72 Scher, F. M., 76 Schizophyllum commune transformation, 94 Schroth, M. N., 82-83 Serine protease, 418 Serratia marcescens chitinase, 101 Seymour, A. B., 43 Shipton, P. J., 76 Siderophores, 346-48, 351-54 see also Iron Simmonds, M., 69 Smith, E. H., 47 Smith, Erwin F., 51 Smith, H. S., 67 Smith, Ralph Eliot, 41-40 early years, 42 introduction, 41

chemodifferentiation, 238southern California, 48-50 University of California, 43-48 Snyder, W. C., 70 Sobemoviruses, 112 Sodium, 275, 278, 280, 283 Soil characteristics effect on jarrah dieback, 212-13 fungistasis, 322, 326 microbes Phytophthora cinnamomi suppression, 213-14 Southern bean mosaic, 113, 115 Sproul, William, 44 Squash mosaic virus, 113, 115 seed transmission, 116 Stone, G. E., 43-44, 46 Stotzky, G., 76 Sugarcane rust, 170 Suslow, T. V., 82 Syringotoxin, 351 Taxol, 242 Taylor, A. L., 68 Taylor, C. B., 68 Temperature Aspergillus, 262 aflatoxin formation, 259-60 Phytophthora cinnamomi, 211-12, 219 rust fungi heat shock effect, 241 infection structure formation, 238-39 Thanatephorus corchorus, 126 cucumeris, 126-27, 129-30, orchidicola, 126 sterigmaticus, 126 Thiamine, 132-33 Thigmodifferentiation, 237-39 Thomashow, L. S., 83 Ti plasmid Agrobacterium pathogenicity basis, 90-92 gene insertion into plants, 18 gene vector, 99 Tobacco mosaic virus, 12, 15-16, 117 inactivation by RNase, 119 Tobacco necrosis virus satellite, 13

Tobacco ringspot virus, 14

plants, 279

cation concentration in young

Tomato

yield carbon dioxide and salt	Virology, changing scene, 11- 23	W
effect, 276	conclusions, 21-22	Waite, M. B., 46
salinity effect, 278	diagnosis, 19-20	Walker, John. Charles, 41-58,
Tomato bushy stunt virus, 13	disease control, 17-18	70
Toxins, 28-31	molecular biology and	early years, 51-52
Triadimefon, 191, 299	novel approaches, 18-	relations with growers, 56
Tridemorph, 201	19	students, 53-54
decrease in activity, 202	disease induction, 16-17	use of language, 55
Tristeza virus, 102	introduction, 11-13	Wisconsin, 53
Trypanosoma hrucei, 392	nomenclature and taxonomy,	Water potential
Turgor, 274	20-21	water salinity, 274
Turnip yellow mosaic virus, 12,	satellite viruses, satellite	Weindling, R., 68
15, 17, 113	RNAs, and viroids, 13	Weller, D. M., 80, 83
Tveit, M., 71	virus replication, 15-16	Wickson, E. J., 48-49
Tyloses, 324, 330	viruslike diseases caused by	Windham, M. T., 83
Tymoviruses, 112	cellular parasites, 17	Wood, R. K. S., 71
Tymovituses, 112	Viruses	Wound tumor virus, 12
	Rhizoctonia, 139	Wright, J. M., 68
U	Viruses, beetle transmission,	Wilgitt, J. Wi., Go
	111-23	X
Uredospores, 239	beetle families	A
appressoria, 237	Chrysomelidae, 113	Xanthomonas
initiation, 236	Coccinellidae, 113	campestris, 420, 423
germ tubes, 235	Curculionidae, 113	campestris, 420, 423
	Meloidae, 114	159
germling, 240-41	beetle vectoring of viruses,	pathogenicity basis studies,
heat shock, 241	114-15	93-94
responses to host surface,	epidemiology, 115-17	campestris pv. citri, 159
	virus acquisition, retention,	campestris pv. curi, 159
host entry, 233	and transmission,	avirulence gene expression,
Uromyces 232 230	and transmission,	
appendiculatus, 232, 239,		97, 148 campestris pv. malvacearum
243	introduction, 111	
appressoria, 237-38, 240,	mechanisms	avirulence genes, 96, 148
242	gross-wounding technique,	campestris pv. oryzae
uredospore, 235-36	117-18	see Bacterial blight of rice
uredospore germling, 238-	selective effect of ribonu-	campestris pv. oryzicola, 361
39, 241	clease, 118-19	campestris pv. phaseoli, 97 campestris pv. vasculorum,
fabae	specificity of viruses,	
uredospores, 236	117	361
Ustilage	translocation, 119-20	campestris pv. vesicatoria
maydis	projections, 120-21	avirulence gene, 97, 148
genetic maps, 388	virus groups, 111	Xylan, 419
violacea	bromoviruses, 112	7
genetic map, 388	comoviruses, 112	Z
mitotic map, 394	other viruses, 112-13	-
**	sobemoviruses, 112	Zoospores
V	tymoviruses, 112	Phytophthora cinnamomi,
Viroids, 14	von Tubeau, Karl, 43	212, 214-16, 220-21
	von Tubeuf, C. F., 67	